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QY 333 KNADNPTMYKQVTCPEKAITAKSGCSR 359
 Db 192 QNADNPSINFNQVTCPELTAKTCKR 218

RESULT 2

Q9JH87 PRELIMINARY; PRT; 219 AA.
 AC Q9JH87; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045176; BAA98046.1; -
 DR HSSP: P43316; ZENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23134 MW; 4BDEF4EC9ACC772D CRC64;

Query Match

Best Local Similarity 37.6%; Score 735; DB 14; Length 219;
 Best Local Similarity 61.7%; Pred. No. 9.6e-39;
 Matches 132; Conservative 28; Mismatches 48; Indels 6; Gaps 4;

QY 148 VSGAGSGEETRYWDCCKPSCSWPGKADVTSPVGSCKNDKGT-LADNNT-QNGCVGSSITCNDQ 205
 Db 9 ISWLSADSGRTTRWDCCKSGCGMEKKNVNDKPIDTCADGTRVASNDTVSGCDGDDG 68
 QY 206 YTCNDNCPWYVSDDLAIFPAASISGSEATWCCACFELTFTSTAVKGMVQVNTGSDLSNTG 265
 Db 69 FMCYDQTFWQVSDLSYGFPAACCGG-ESGACCCGCTELTFTSGPVGKMMVQVNTGSDLSNTG 127
 QY 266 DLGSNTGAHPDLQMPGGGVGIYNGCATQWGAPTDGMGARYGVSSASDCSNLPSALQAGC 325
 Db 128 DLGSN---QFDLAIPEGGVGIYNGCTAQSGAPSDGMSRYGVSRSRSCQSLPSGLQAGC 184
 QY 326 KMRFGMRKADNPTMYKQVTCPEKAITAKSGCSR 359
 Db 185 QMRFDWQNDNPSINFNSOVSCPELITAKTCKR 218

RESULT 3

Q9JH84 PRELIMINARY; PRT; 220 AA.
 AC Q9JH84; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045179; BAA98049.1; -
 DR HSSP: P43316; ZENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CRC64;

Query Match 37.6%; Score 735; DB 14; Length 220;
 Best Local Similarity 64.3%; Pred. No. 9.6e-39;
 Matches 133; Conservative 21; Mismatches 47; Indels 6; Gaps 4;

QY 155 NGETTRYWDCCKPSCSWPGKADVTSPVGSCKNDKGT-LADNNT-QNGCVGSSITCNDQ 212
 Db 17 SGKTRRYWDCCKKASCMEKKAATVPTDGTGDTTRLASNDTVSSCDGGDGYMCYDQ 76
 QY 213 PMVVSDDLAYGFAAASISGSEATWCCACFELTFTSTAVKGMVQVNTGSDLSNTG 272
 Db 77 PMAVNDSVAAGFAAACCGG-ETGACCCCTELTFTSGPVGKMMVQVNTGSDLSN-- 133
 QY 273 AHFDLQMPGGGVGIYNGCATQWGAPTDGMGARYGVSSASDCSNLPSALQAGCKMRFGWF 332
 Db 134 -QFDLAIPEGGVGIYNGCTAQSGAPADGMSRYGVSRSRSCQSLPSGLQAGCQMRFDWF 192
 QY 333 KNADNPTMYKQVTCPEKAITAKSGCSR 359
 Db 193 QNADNPSINFNQVTCPELTAKTCKR 219

RESULT 4

Q9JH83 PRELIMINARY; PRT; 220 AA.
 AC Q9JH83; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB045167; BAA98037.1; -
 DR EMBL: AB045166; BAA98036.1; -
 DR HSSP: P43316; ZENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 220 AA; 23108 MW; 97736D831BCFA5F3 CRC64;

Query Match 37.5%; Score 734; DB 14; Length 220;
 Best Local Similarity 63.8%; Pred. No. 1.1e-38;
 Matches 132; Conservative 23; Mismatches 46; Indels 6; Gaps 4;

QY 155 NGETTRYWDCCKPSCSWPGKADVTSPVGSCKNDKGT-LADNNT-QNGCVGSSITCNDQ 212
 Db 17 SGKTRRYWDCCKSGCGMEKKAADVSKPIDTCADGTRVASNDTVSGCDGDDGYMCYDQ 76
 QY 213 PMVVSDDLAYGFAAASISGSEATWCCACFELTFTSTAVKGMVQVNTGSDLSNTG 272
 Db 77 PMGVNDSVALGFAAASISGGERAA-CCNCYELTFTSGPVGKMMVQVNTGSDLSN-- 133
 QY 273 AHFDLQMPGGGVGIYNGCATQWGAPTDGMGARYGVSSASDCSNLPSALQAGCKMRFGWF 332
 Db 134 -QFDLAIPEGGVGIYNGCTAQSGAPADGMSRYGVSRSRSCQSLPSGLQAGCQMRFDWF 192
 QY 333 KNADNPTMYKQVTCPEKAITAKSGCSR 359
 Db 193 QNADNPSINFNQVTCPELTAKTCKR 219

RESULT 5

Q9JH91 PRELIMINARY; PRT; 219 AA.
 AC Q9JH91;

Query Match	37.5%	Score 733;	DB 14;	Length 219;
Best Local Similarity	64.3%	Pred. No. 1.3e-38;		
Matches 133;	Conservative 21;	Mismatches 47;	Indels 6;	Gaps 4;

RESULT 6
Q9JH95
ID Q9JH95 PRELIMINARY; PRT; 217 AA

Query Match	37.3%;	Score 730;	DB 14;	Length 217;
Best Local Similarity	63.3%;	Pred. No. 1.9e-38;		
Matches 131;	Conservative 24;	Mismatches 46;	Indels 6;	Gaps 4

QY 155 NGEITRRYMDCKSPGSGRADYTS PVGSCNKGDKGT-LADPNT-QNGCVGSSSYTCNDNQ 212
:::|||||
Db 14 SGKTRRYMDCKSGSGEALADVSKRIDTCAKDGTRRVASVDYVSGCGDGDGFGMCYDQT 73
14

RESULT 7
Q9JH90
ID Q9JH90 PRELIMINARY; PRT; 219 AA

Query Match	37.2%	Score 727;	DB 14;	Length 219;
Best Local Similarity	62.3%	Pred. No. 3e-38;		
Matches 129; Conservative	28;	Mismatches	44;	Indels 6; Gaps 4

RESULT 8
Q9JH88
ID Q9JH88 PRELIMINARY; PRT; 219 AA

AC Q50N09,
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onoike K., Ohkuma M., Moriya S., Kudo T.:
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic

RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045175; BAA98045.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23030 MW; 179BF1344C6D7024 CRC64;

Query Match 37.2%; Score 727; DB 14; Length 219;
 Best Local Similarity 62.8%; Pred. No. 3e-38;
 Matches 130; Conservative 25; Mismatches 46; Indels 6; Gaps 4;

OY 155 NGETTRVWDCCPSCMPGKADVTSPVGSCKNDGKT-LADNNT-QNGCVGSSSYTCNDNQ 212
 DB 16 SGTTRVWDCCCKSGCMERKANVDKPIDTCADGTRVASNDTVKSGCDGDFMCYDQT 75
 OY 213 PMVVSDDLAVGFPAASISGSEATWCCACPELFTSTAVKGMVYVNTGSDLSGNTG 272
 DB 76 PMQVSDSLSTGFPAALACCGG-ESGACCCGCELTFTTSGPVNKKMTVQITNTGGDLGSN-- 132
 OY 273 AHFDLQMPGGVGIYNGCATQWGAPTDGMGARVGVSSASDSCNLPALQAGCKMRFGMF 332
 DB 133 -QFDLAIPEGGVGIYNGCTSSGAPADGWSRGVSSRSSECSQLPBLQAGCMRFDWF 191
 OY 333 KNADNPMTYKQVTCPEKAITAKSGCSR 359
 DB 192 ANADNPINFTNVKCPSELIATKNCNR 218

RESULT 9

OY 09JH89 PRELIMINARY; PRT; 219 AA.
 AC 09JH89;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RL protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045174; BAA98044.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23033 MW; CA295CADBF393199 CRC64;

Query Match 37.0%; Score 724; DB 14; Length 219;
 Best Local Similarity 62.3%; Pred. No. 4.6e-38;
 Matches 129; Conservative 27; Mismatches 45; Indels 6; Gaps 4;

OY 155 NGETTRVWDCCPSCMPGKADVTSPVGSCKNDGKT-LADNNT-QNGCVGSSSYTCNDNQ 212
 DB 16 SGTTRVWDCCCKSGCMERKANVDKPIDTCADGTRVASNDTVKSGCDGDFMCYDQT 75
 OY 213 PMVVSDDLAVGFPAASISGSEATWCCACPELFTSTAVKGMVYVNTGSDLSGNTG 272
 DB 76 PMQVSDSLSTGFPAALACCGG-ESGACCCGCELTFTTSGPVNKKMTVQITNTGGDLGSN-- 132
 OY 273 AHFDLQMPGGVGIYNGCATQWGAPTDGMGARVGVSSASDSCNLPALQAGCKMRFGMF 332
 DB 133 -QFDLAIPEGGVGIYNGCTSSGAPADGWSRGVSSRSSECSQLPBLQAGCMRFDWF 191
 OY 333 KNADNPMTYKQVTCPEKAITAKSGCSR 359
 DB 192 ANADNPINFTNVKCPSELIATKNCNR 218

RESULT 10

OY 09JH94 PRELIMINARY; PRT; 221 AA.
 AC 09JH94;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RL protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045169; BAA98039.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 221 AA; 23220 MW; 8A84CEB0A8C6372 CRC64;

Query Match 36.9%; Score 721; DB 14; Length 221;
 Best Local Similarity 60.9%; Pred. No. 7.2e-38;
 Matches 126; Conservative 29; Mismatches 46; Indels 6; Gaps 4;

OY 155 NGETTRVWDCCPSCMPGKADVTSPVGSCKNDGKT-LADNNT-QNGCVGSSSYTCNDNQ 212
 DB 17 SGTTRVWDCCCKSGCMERKANVDKPIDTCADGTRVASNDTVKSGCDGDFMCYDQT 76
 OY 213 PMVVSDDLAVGFPAASISGSEATWCCACPELFTSTAVKGMVYVNTGSDLSGNTG 272
 DB 77 PMAVNDSTSLGFPAALAVGSGEKA-CCQCYELFTTSGPVNKKMTVQITNTGGDLGSN-- 133
 OY 273 AHFDLQMPGGVGIYNGCATQWGAPTDGMGARVGVSSASDSCNLPALQAGCKMRFGMF 332
 DB 134 -QFDLAIPEGGVGIYNGCTSSGAPADGWSRGVSSRSSECSQLPBLQAGCMRFDWF 192
 OY 333 KNADNPMTYKQVTCPEKAITAKSGCSR 359
 DB 193 QNADNPINFTNVKCPSELIATKNCNR 219

RESULT 11

OY 09JH93 PRELIMINARY; PRT; 220 AA.
 AC 09JH93;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RL protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045170; BAA98040.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 220 AA; 23091 MW; 35F174F9B79C2D65 CRC64;

Query Match 36.6%; Score 715; DB 14; Length 220;
 Best Local Similarity 62.1%; Pred. No. 1.7e-37;

Matches 128; Conservative 23; Mismatches 49; Indels 6; Gaps 4;

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OY 156 GETTRVWDCCPSCSPGKADVTSPVGSCNKGKT-LADNNT-ONGCVGSSYTCNDNQ 213
    |||||
DB 18 GRTTRVWDCCGSGGEMKAVNDKPIDTCAKDGTTTAVASNDTVKSGCDGEGYMCYDQ 77
OY 214 WVVSDDLAVGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTGA 273
    |||||
DB 78 WGVVDSFALGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTGA 133
OY 274 HFDLQMPGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 333
    |||||
DB 134 QFDLAIPEGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 193
OY 334 NADNPTMTYKQVTCPKAITAKSGCSR 359
    |||||
DB 194 NADNPTMTYKQVTCPKAITAKSGCSR 219

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RESULT 12

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OY 09JH85 PRELIMINARY; PRT; 218 AA.
AC 09JH85;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045178; BAA98048.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN.1.
SQ SEQUENCE 218 AA; 22680 MW; A600FF5B990AD43 CRC64;

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Query Match 36.5%; Score 714.5; DB 14; Length 218;
 Best Local Similarity 60.4%; Pred. No. 1.8e-37;
 Matches 125; Conservative 30; Mismatches 47; Indels 5; Gaps 3;

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OY 155 NGETTRVWDCCPSCSPGKADVTSPVGSCNKGKT-LADNNT-ONGCVGSSYTCNDNQ 213
    |||||
DB 16 DGRTRVWDCCGSGGEMKAVNDKPIDTCAKDGTTTAVASNDTVKSGCDGEGYMCYDQ 75
OY 214 WVVSDDLAVGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTGA 273
    |||||
DB 76 RAVVDSYALGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTGA 131
OY 274 HFDLQMPGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 333
    |||||
DB 134 QFDLAIPEGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 191
OY 334 NADNPTMTYKQVTCPKAITAKSGCSR 360
    |||||
DB 192 NADNPTMTYKQVTCPKAITAKSGCSR 218

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RESULT 13

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OY 09JH96 PRELIMINARY; PRT; 220 AA.
AC 09JH96;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.

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OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]

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RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045165; BAA98035.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN.1.
SQ SEQUENCE 220 AA; 23148 MW; 4F0552F8B8D269D5 CRC64;

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Query Match 36.4%; Score 712; DB 14; Length 220;
 Best Local Similarity 62.3%; Pred. No. 2.6e-37;
 Matches 129; Conservative 23; Mismatches 49; Indels 6; Gaps 4;

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OY 155 NGETTRVWDCCPSCSPGKADVTSPVGSCNKGKT-LADNNT-ONGCVGSSYTCNDNQ 212
    |||||
DB 17 SGRTTRVWDCCGSGGEMKAVNDKPIDTCAKDGTTTAVASNDTVKSGCDGEGYMCYDQ 76
OY 213 PVVVSDDLAVGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTG 272
    |||||
DB 77 PRAVNDYALGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTG 133
OY 273 AHFDLQMPGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 332
    |||||
DB 134 QFDLAIPEGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 192
OY 333 KNAADNPTMTYKQVTCPKAITAKSGCSR 359
    |||||
DB 193 KNAADNPTMTYKQVTCPKAITAKSGCSR 219

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RESULT 14

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OY 09JH86 PRELIMINARY; PRT; 219 AA.
AC 09JH86;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045177; BAA98047.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN.1.
SQ SEQUENCE 219 AA; 23158 MW; ECD686EAB8BD1D1 CRC64;

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Query Match 36.3%; Score 711; DB 14; Length 219;
 Best Local Similarity 60.9%; Pred. No. 3e-37;
 Matches 126; Conservative 27; Mismatches 48; Indels 6; Gaps 4;

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OY 155 NGETTRVWDCCPSCSPGKADVTSPVGSCNKGKT-LADNNT-ONGCVGSSYTCNDNQ 212
    |||||
DB 16 SGRTTRVWDCCGSGGEMKAVNDKPIDTCAKDGTTTAVASNDTVKSGCDGEGYMCYDQ 75
OY 213 PVVVSDDLAVGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTG 272
    |||||
DB 76 PRAVNDYALGFAAASISGSEBATEWCCAFELTFTSTAVKGMVQVNTGSDLSNTG 132
OY 273 AHFDLQMPGGVGIYNGCATQMGAPTDGKARVGVSSASDCSNLPSALQACCKRFGWF 332
    |||||

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Db      133 -OFDLAIPGGVIGTNGCTAGSAPSDGSRVGVSSRSBSCQ.PSGLQAGCCQWRFDWF 191
QY      333 KNADNPTMYKQVTCPKAITAKSGCSR 359
Db      192 QNADNPNINFSSVRCPAEIIAKTNCNR 218

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RESULT 15

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ID      093782      PRELIMINARY;      PRT;      305 AA.
AC      093782;
DT      01-MAY-1999 (TRENBLREL. 10, Created)
DT      01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT      01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE      Endoglucanase.
GN      EGL3.
OS      Humicola grisea var. thermoides.
OC      Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX      NCBI_TaxID=5528;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=IFO9854;
RX      MEDLINE=9914540; PubMed=9990729;
RA      Takashima S., Iikura H., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT      "Comparison of gene structures and enzymatic properties between two
RT      endoglucanases from Humicola grisea.";
RL      J. Biotechnol. 67:85-97(1999).
DR      EMBL; AB003107; BAK74956.1; -.
DR      HSSP; P4316; 2ENG.
DR      InterPro; IPR000254; CBD_fungal.
DR      InterPro; IPR000334; GH_45.
DR      Pfam; PF00734; CBM_1; 1.
DR      Pfam; PF02015; Glyco_hydro_45; 1.
DR      ProDom; PD001821; CBD_fungal; 1.
DR      SMART; SM00236; ECD; 1.
DR      ProSITE; PS00562; CBD_FUNGAL; 1.
DR      PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
SQ      SEQUENCE 305 AA; 32174 MW; 28C979D6D6DCD771D CRC64;

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Query Match      34.9%; Score 683.5; DB 3; Length 305;
Best Local Similarity 57.2%; Pred. No. 2.1e-35;
Matches 119; Conservative 32; Mismatches 50; Indels 7; Gaps 3;

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QY      153 SGNGETRYWDCCPKSCSPGKADVTSPVGSCKNDKTLADNNTONGC-VGGSSYTCNDN 211
Db      21 AADCKSTRYWDCCPKSCSPGKAKAPVNPVPSCNANFQRLTFDAKSGCEPGVAAYSCADQ 80
QY      212 QPWTVSDDLAVGFPAASISGSEATWCCAFELFTSTAIVKSKMNVQVNTGSDIGSNT 271
Db      81 TPWAVNDPFAFGPAATSIAGSNENAGWCACCYELFTSGPVA GKMMVQSTSTGDLGSN- 139
QY      272 GAHPDLQMPGGGAGIYNGCATOWGAPTDGWCARYGVSSASDCSNLPSALQAGCKWRFGW 331
Db      140 --HFDLNIPIGGGVIGTNGCTAGSAPSDGSRVGVSSRSBSCQ.PSGLQAGCCQWRFDWF 194
QY      332 FKADNPTMYKQVTCPKAITAKSGCSR 359
Db      195 FKADNPNINFSSVRCPAEIIAKTNCNR 222

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Search completed: June 18, 2003, 17:14:24
 Job time : 31.1827 secs